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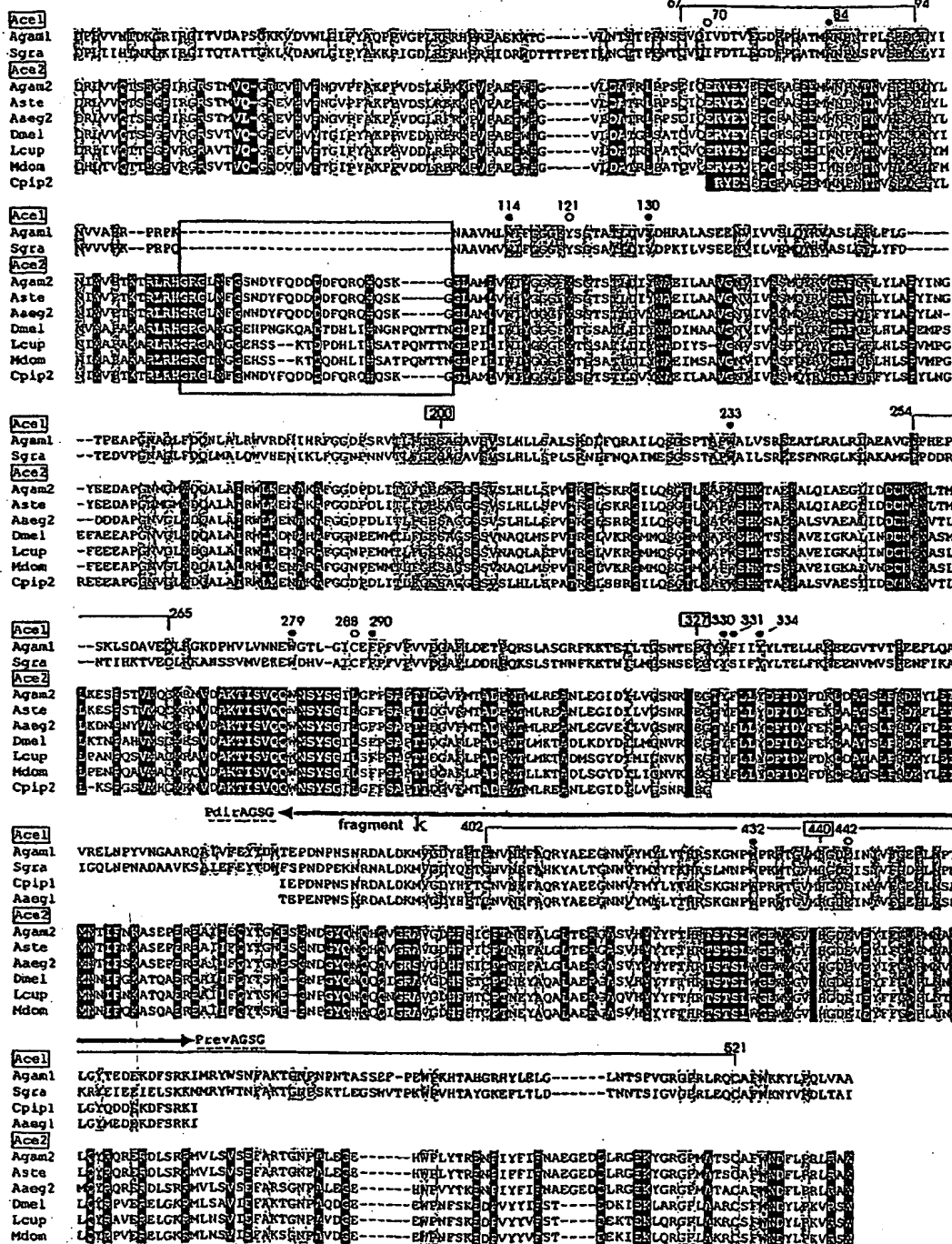


FIGURE 1

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A

	1	80
Ae alb	TEPDNPNSNR DALDKMVG DY HFTCNVNEFA QRYABEGNNV YMYLYTHRSK GNPWPRMTGV MHGDEINYPF GEPLNGLGY	
Ae aeg	TEPDNPNSNR DALDKMVG DY HFTCNVNEFA QRYABEGNNV YMYLYTHRSK GNPWPRMTGV MHGDEINYPF GEPLNGLGY	
An alb	TEPDNPNSNR DALDKMVG DY HFTCNVNEFA QRYABEGNNV YMYLYTHRSK GNPWPRMTGV MHGDEINYPF GEPLNGLGY	
An gam	TEPDNPNSNR DALDKMVG DY HFTCNVNEFA QRYABEGNNV YMYLYTHRSK GNPWPRMTGV MHGDEINYPF GEPLNGLGY	
An fun	TEPDNPNSNR DALDKMVG DY HFTCNVNEFA QRYABEGNNV YMYLYTHRSK GNPWPRMTGV MHGDEINYPF GEPLNGLGY	
An nil	TEPDNPNSNR DALDKMVG DY HFTCNVNEFA QRYABEGNNV YMYLYTHRSK GNPWPRMTGV MHGDEINYPF GEPLNGLGY	
An sac	TEPDNPNSNR DALDKMVG DY HFTCNVNEFA QRYABEGNNV YMYLYTHRSK GNPWPRMTGV MHGDEINYPF GEPLNGLGY	
An pse	TEPDNPNSNR DALDKMVG DY HFTCNVNEFA QRYABEGNNV YMYLYTHRSK GNPWPRMTGV MHGDEINYPF GEPLNGLGY	
Cx Pip	TEPDNPNSNR DALDKMVG DY HFTCNVNEFA QRYABEGNNV YMYLYTHRSK GNPWPRMTGV MHGDEINYPF GEPLNGLGY	

	81	91
Ae alb	TEDEKDFSRK I	
Ae aeg	TEDEKDFSRK I	
An alb	TEDEKDFSRK I	
An gam	TEDEKDFSRK I	
An fun	TEDEKDFSRK I	
An nil	TEDEKDFSRK I	
An sac	TEDEKDFSRK I	
An pse	TEDEKDFSRK I	
Cx Pip	TEDEKDFSRK I	

B

	20	40	60	80
Acel-SLAB	ATGGAACCGGACAAACCGGACAGCAACCGTGACGGCTGGACAAGATGGTGGGGATTATCACTTCACCTGCAACGCTGAA			
Acel-SR	ATGGAACCGGACAAACCGGACAGCAACCGTGACGGCTGGACAAGATGGTGGGGATTATCACTTCACCTGCAACGCTGAA			

	100	120	140	160
Acel-SLAB	CGAATTGCGCCAGCGGTACGCGGAGGAGGCAACAACGTTTTCATGTACCTGTACACGCACAGAAGCAAGGAAATCCCT			
Acel-SR	CGAATTGCGCCAGCGGTACGCGGAGGAGGCAACAACGTTTTCATGTACCTGTACACGCACAGAAGCAAGGAAATCCCT			

	180	200	220	240
Acel-SLAB	GGCCGAGGTGGACGGCGTGATGCACGGCGACGAGATCAACTACGTGTTTGGCGAACCGCTGAACCTGGGCCCTCGGCTAC			
Acel-SR	GGCCGAGGTGGACGGCGTGATGCACGGCGACGAGATCAACTACGTGTTTGGCGAACCGCTGAACCTGGGCCCTCGGCTAC			

	260
Acel-SLAB	CAGGACGACGAGAAGGACTTTAGCCGGAAAATT
Acel-SR	CAGGACGACGAGAAGGACTTTAGCCGGAAAATT

C

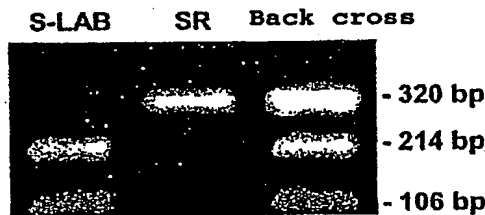


FIGURE 2

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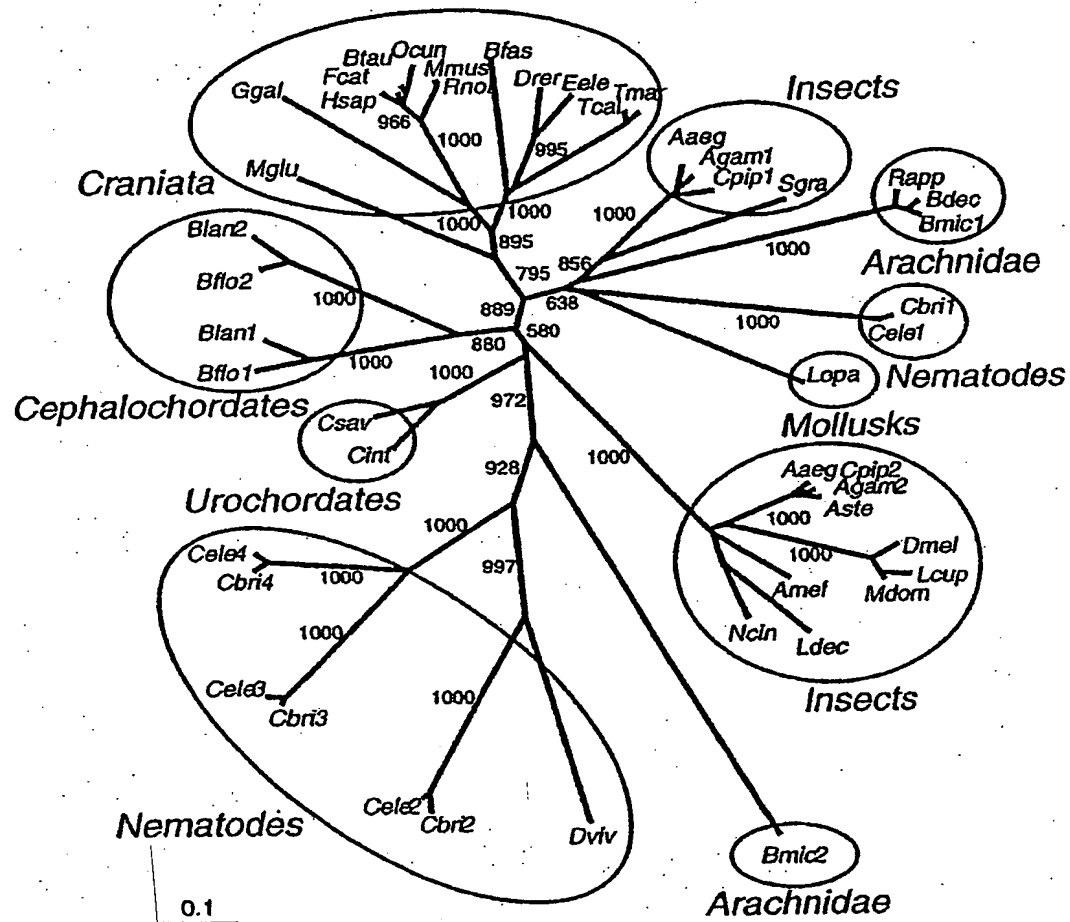


FIGURE 3

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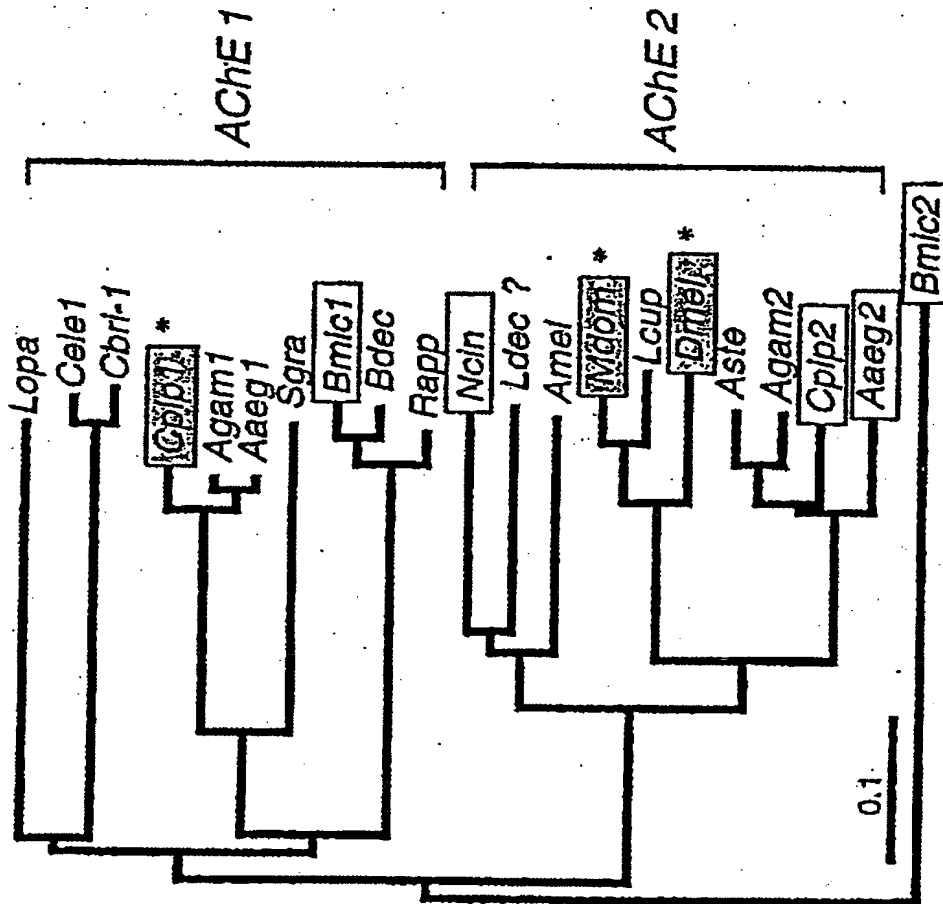


FIGURE 4

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1
SR MEIRGLITRL LGPCHLRHLI LCSLGLYSIL VQSVHCRHHD IGSSVAHQLG SKYSQSSSL SSSQSSSLA SEATLNKDSO 80
S-LAB MEIRGLITRL LGPCHLRHLI LCSLGLYSIL VQSVHCRHHD IGSSVAHQLG SKYSQSSSL SSSQSSSLA SEATLNKDSO

81
SR AEFTPYIGHG DSVRIVDAL GLTEREHHS TTRRRGLTR RESSSDATOS DPLVITTDKG KIRGTTLEAP SGKKVDAMNG 160
S-LAB AEFTPYIGHG DSVRIVDAL GLTEREHHS TTRRRGLTR RESSSDATOS DPLVITTDKG KIRGTTLEAP SGKKVDAMNG

161
SR IPYAQPPLGP LRFRHPRPAE RMTGVLMATE PPRSCVQIVD TVFGDFPGAT MWNPTPLSE DCLYINVVVP RPRPKAAVM 240
S-LAB IPYAQPPLGP LRFRHPRPAE RMTGVLMATE PPRSCVQIVD TVFGDFPGAT MWNPTPLSE DCLYINVVVP RPRPKAAVM

241
SR LWFPGGFFYS GTATLDVYDH RTLASEENVI VVSLQYEVAS LGFLFLGTPE APGNAGLFDQ NLALRWVRON IHRFGGDFSR 320
S-LAB LWFPGGFFYS GTATLDVYDH RTLASEENVI VVSLQYEVAS LGFLFLGTPE APGNAGLFDQ NLALRWVRON IHRFGGDFSR

321
SR VTLFGESAGA VSVSLHLLSA LSRDLQRAI LQSGSPTAPW ALVSREZATL RALRLAEAVN CPHDATEKLSO AVECLRTADP 400
S-LAB VTLFGESAGA VSVSLHLLSA LSRDLQRAI LQSGSPTAPW ALVSREZATL RALRLAEAVN CPHDATEKLSO AVECLRTADP

401
SR NELVDNEWGT LGICEFFFPV VVDGAFDDET PQRSASGRF KKTDLITGSM TEEGYFFIY YLTLLRKEE GVTVTREEF 480
S-LAB NELVDNEWGT LGICEFFFPV VVDGAFDDET PQRSASGRF KKTDLITGSM TEEGYFFIY YLTLLRKEE GVTVTREEF

481
SR QAVRELNPYV NGAARQAIVF EYTDWIEPDN PMSNRDALDE MVDGYHFTCN VNEFAQRYAE EGNVFMVLY THRSKGNPWP 560
S-LAB QAVRELNPYV NGAARQAIVF EYTDWIEPDN PMSNRDALDE MVDGYHFTCN VNEFAQRYAE EGNVFMVLY THRSKGNPWP

561
SR RMTGVMHGDE INTVGEPLN SALGYQDEK DFSRKIMRYN SNFAKTGNPN PSTPSVDLPE WPKHTANGRH YLELGIAVTF 640
S-LAB RMTGVMHGDE INTVGEPLN SALGYQDEK DFSRKIMRYN SNFAKTGNPN PSTPSVDLPE WPKHTANGRH YLELGIAVTF

641
SR VGRGPRLRQC AFWKYLPQL VAATSNLQVT PAPSVPCESS STSYRSTLL IVTLLLVTRF KI 702
S-LAB VGRGPRLRQC AFWKYLPQL VAATSNLQVT PAPSVPCESS STSYRSTLL IVTLLLVTRF KI

Figure 5

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1 80
S-LAB M E I R G L I T R L L G P C H L R H L I L C S L G L Y
SR ATGGAGATCCGAGGCCAATAACCGATTACTGGGTCCATGTCACCTGCGACATCTGATACTGTGCACTTTGGGGCTGTA

160
S-LAB S I L V Q S V H C R H H D I G S S V A H Q L G S K Y S
SR CTCCATCCTCGTGCAGTCGGTCCATTGCCGGCATCATGACATCGGTAGTTCGGTGGCACACCAGCTAGGATCGAAATACT

240
S-LAB Q S S S L S S S S Q S S S S L A E E A T L N K D S D
SR CACAATCATCCTCGTTATCGTCATCCTCGCAATCGTCATCGTTCGTTAGCTGAAGAGGCCACGCTGAATAAGATTGAGAT

320
S-LAB A F F T P Y I G H G D S V R I V D A E L G T L E R E H
SR GCATTTTTTACACCATATATAGGTCACGGAGATTCTGTTGCAATTGTAGATGCCGAATTAGGTACATTAGAGCGCGAGCA

400
S-LAB I H S T T T R R R G L T R R E S S S D A T D S D P L V
SR TATCCATAGCACTACGACCCCGCGGCGTGGCCTGACCCGGAGGGAGTCCAGCTCCGATGCCACCGACTCGGACCCCACTGG

Primer Ex3dir
480
S-LAB I T T D K G K I R G T T L E A P S G K K V D A W M G
SR TCATAACGACGGACAAGGGCAAATCCGTGGAACGACACTGGAAGCGCTAGTGGAAGAAGGTGGACGCATGGATGGGC

560
S-LAB I P Y A Q P P L G P L R F R H P R P A E R W T G V L N
SR ATTCGTAGCGGAGCCCGCTGGGTCCGCTCCGGTTTCGACATCCGCGACCCCGCGAAAGATGGACCGGTGTGCTGAA

640
S-LAB A T K P P N S C V Q I V D T V F G D F P G A T M W N P
SR CGCGACCAAACCGCCCACTCCTGCGTCCAGATCGTGGACACCGTGTTCGGTGACTTCCGGGGGCCACCATGTGGAACC

720
S-LAB N T P L S E D C L Y I N V V V P R P R P K N A A V M
SR CGAACACACCGCTCTCGGAGGACTGTCTGTACATCAACGTGGTCCGTCACGGCCAGGCCCAAGATGCCGCCGTCTATG

800
S-LAB L W I F G G G F Y S G T A T L D V Y D H R T L A S E E
SR CTGTGGATCTTCGGGGGTGGCTTCTACTCCGGGACTGCCACGCTGGACGTGTACGACCATCGGACGCTGGCCTCGGAGGA

880
S-LAB N V I V V S L Q Y R V A S L G F L F L G T P E A P G N
SR GAACGTGATCGTAGTTTCGCTGCAGTACCGTGTGCAAGTCTTGGGTTCTCTTCTGCGGCACACCGGAGGCACCCGGTA

960
S-LAB A G L F D Q N L A L R W V R D N I H R E G G D F S R
SR AC~~CGGGGCTGTTGATCAGAAC~~CTGGCACTGAGATGGGTCCGCGACACATCCACCGGTTCCGGGGTGACCCCTCGCGG

Primer Ex3rev
1040
S-LAB V T L F G E S A G A V S V S L H L L S A L S R D L F Q
SR GTCACACTGTTCCGCGAGAGCGCCGAGCGGTCTCGGTTTCGCTGCACCTGCTGTCCGGGCTCTCGCGGGACCTGTTC

Figure 6A

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1120
S-LAB  R A I L Q S G S P T A P W A L V S R E E A T L R A L R
SR      GCGGGCCATCCTCCAGAGTGGCTCCCCGACGGCCCGTGGGCGCTGGTTTCGCGGAAGAAGCTACGCTTAGAGCTCTTC
-----A-----

1200
S-LAB  L A E A V N C P H D A T K L S D A V E C L R T K D P
SR      GTCTGGCGAGGCCGTCAACTGTCCGACGATGCGACCAAGCTGAGCGATGCCGTGGAATGCCCTGCGAACCAGGATCCG
-----T-----

1280
S-LAB  N E L V D N E W G T L G I C E F P F V P V V D G A P L
SR      AACGAGCTGGTGCACAACGAGTGGGGCAGCTGGGGATCTGCGAGTTTCGGTTTCGGTTTGGGACGGAGCCTTCCT
-----T-----

1360
S-LAB  D E T P Q R S L A S G R F K K T D I L T G S N T E E G
SR      CGATGAGACACCGCAGCGTTTCGTTGGCCAGCGGCGCTTCAAGAAAACGGACATCCTGACCGGCAGCAACCCGAGGAGG
-----T-----

1440
S-LAB  Y Y F I I Y Y L T E L L R K E E G V T V T R E E F L
SR      GTTACTACTTTATCATTTACTATCTAACCGAAGTGTCTAGGAAGAGGAAGGGGTACCGGTAAACCGGAGGAGTTCCTA
-----C-----

1520
S-LAB  Q A V R E L N P Y V N G A A R Q A I V F E Y T D W I E
SR      CAGGCGCTCCGGGAGTTGATCCGTACGTGAACGGTGCCCGCCCGCAGGCCATCGTGTTCGAGTACACGGACTGGATTGA
-----C-----

1600
S-LAB  P D N P N S N R D A L D K M V G D Y H F T C N V N E F
SR      ACCGGACAACCCGAACAGCAACCGTGACGCGCTGGCAAGATGGTCGGGGATTATCACTTCACCTGCAACGTGAAGCAAT
-----G-----

1680
S-LAB  A Q R Y A E E G N N V F M Y L Y T H R S K G N P W P
SR      TCGCCACGCGGTACGCCGAGGAGGGCAACAACGTGTTTCATGTACCTGTACACGCACAGAAGCAAGGAATCCCTGGCCG
-----T-----

1760
S-LAB  R W T G V M H G D E I N Y V F G E P L N S A L G Y Q D
SR      AGGTGGACCGGCGTGATGCACGGGACGAGATCAACTACGTGTTTGGCGAACCGCTGAAGTCCGCCCTCGGCTACAGGA
-----T-----

1840
S-LAB  D E K D F S R K I M R Y W S N F A K T G N P N P S T P
SR      CGACGAGAAGGACTTTAGCCGGAAAATTATGCGATACTGGTCCAACTTTGCCAAGACTGGCAATCCCAACCCGAGTACGC
-----A-----

1920
S-LAB  S V D L P E W P K H T A H G R H Y L E L G L N T T F
SR      CGAGCGTGGACCTGCCCGAATGGCCCAAGCACACCGCCACGGACGACACTATCTGGAGCTGGGACTGAACACGACCTTC
-----A-----

2000
S-LAB  V G R G P R L R Q C A F W K K Y L P Q L V A A T S N L
SR      GTGGGACGGGGCCACGATTGCGGCAGTGCGCTTTCTGGAAGAAATATTTGCGCAACTAGTAGCAGCTACCTCTAACCT
-----A-----

2080
S-LAB  Q V T P A P S V P C E S S S T S Y R S T L L L I V T L
SR      CCAAGTAACTCCCGCGCTAGCGTACCTTGCAGAAAGCAGCTCAACATCTTATCGATCCACTCTACTTCTAATAGTCACAC
-----A-----

2109
S-LAB  L L V T R F K I *
SR      TACTTTTAGTAACGCGGTTCAAGATTAA
-----A-----

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Figure 6B

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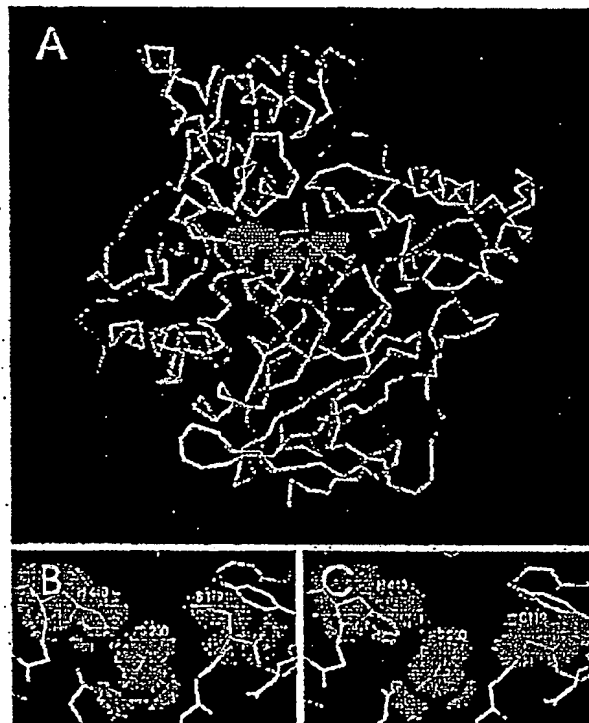


Figure 7

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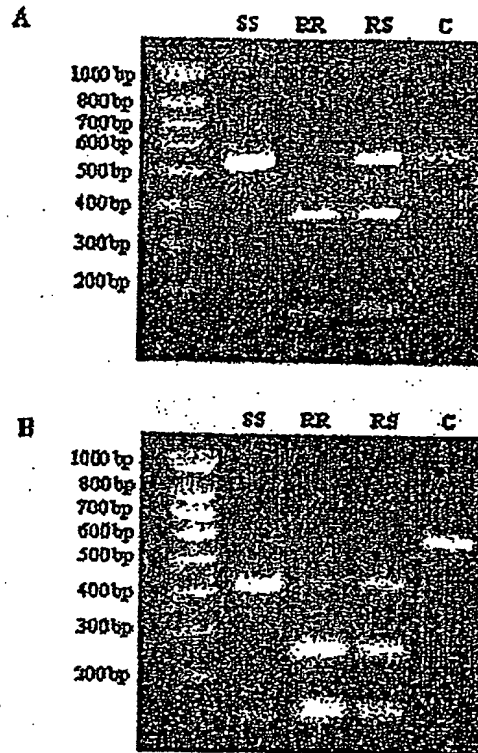


Figure 8

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[illegible]

Figure 9A

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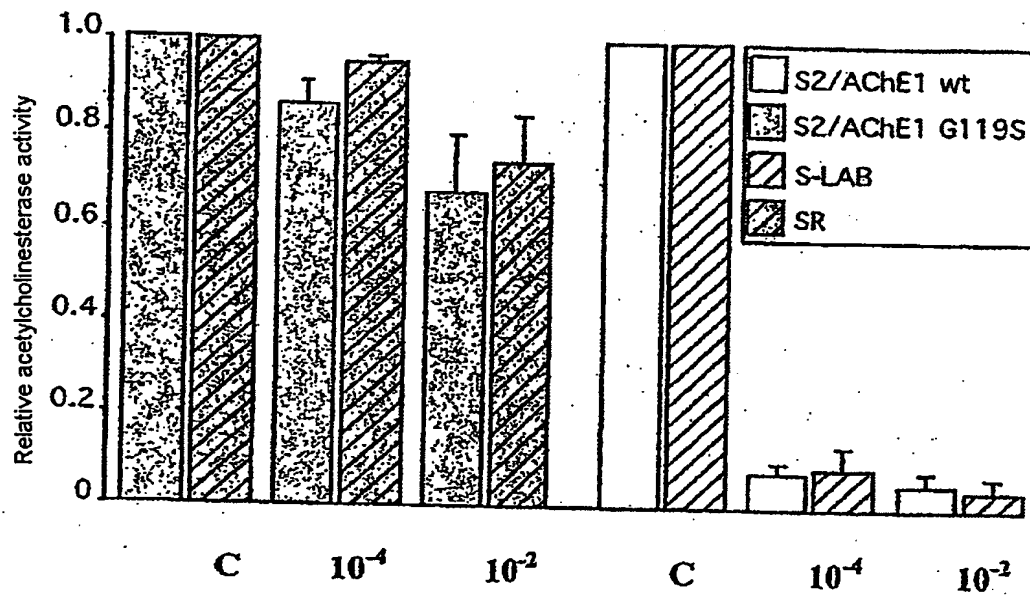


Figure 10

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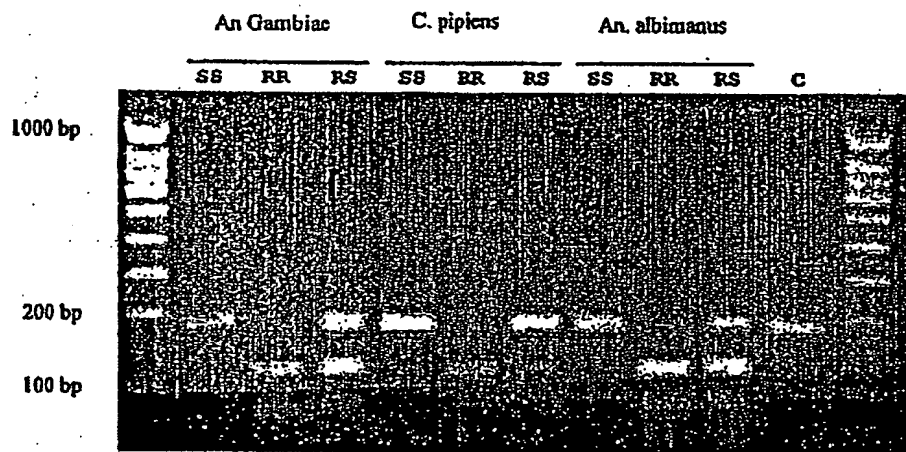


FIGURE 11

Assay for inhibition with propoxur

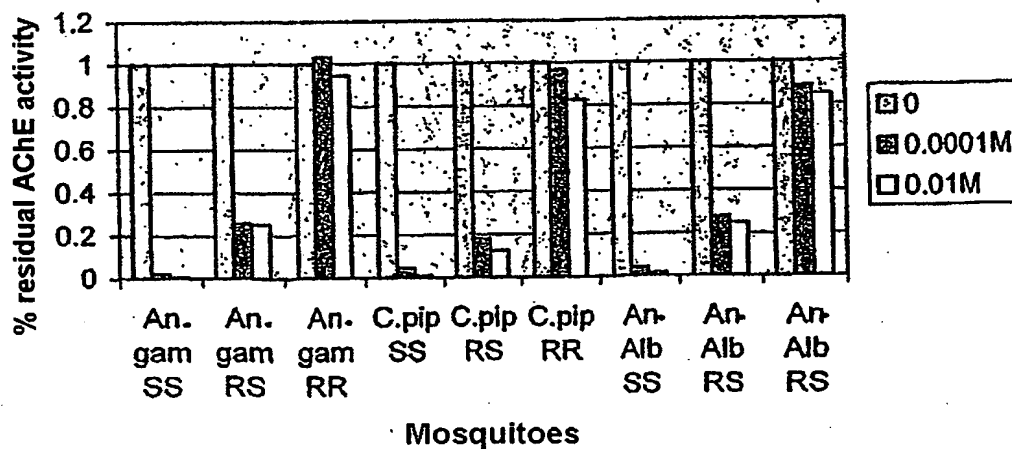


FIGURE 12



FIGURE 14